

10/539634

RAW SEQUENCE LISTING

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Application Serial Number: 10/539634
Source: PCT
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PCT

RAW SEQUENCE LISTING

DATE: 06/27/2005

PATENT APPLICATION: US/10/539,634

TIME: 10:38:37

Input Set : A:\SEQ LIST WSU-10 (US).txt

Output Set: N:\CRF4\06272005\J539634.raw

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3 <110> APPLICANT: CARLOCK, Leon
4   CYPHER, Maria
6 <120> TITLE OF INVENTION: Bioactive Peptides and Unique IRES Elements from
7   Myelin Proteolipid Protein PLP/DM20
9 <130> FILE REFERENCE: 2872-0010
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/539,634
C--> 12 <141> CURRENT FILING DATE: 2005-06-16
14 <150> PRIOR APPLICATION NUMBER: PCT/US03/39873
15 <151> PRIOR FILING DATE: 2003-12-16
17 <150> PRIOR APPLICATION NUMBER: US 60/433,573
18 <151> PRIOR FILING DATE: 2002-12-16
20 <160> NUMBER OF SEQ ID NOS: 40
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 850
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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40 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe
41          20          25          30
43 tgt ggc tgt gga cat gaa gcc ctc act ggc aca gaa aag cta att gag      144
44 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu
45          35          40          45
47 acc tat ttc tcc aaa aac tac caa gac tat gag tat ctc atc aat gtg      192
48 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
49          50          55          60
51 atc cat gcc ttc cag tat gtc atc tat gga act gcc tct ttc ttc ttc      240
52 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
53 65          70          75          80
55 ctt tat ggg gcc ctc ctg ctg gct gag ggc ttc tac acc acc ggc gca      288
56 Leu Tyr Gly Ala Leu Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala
57          85          90          95
59 gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc      336
60 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
61          100          105          110
63 ctg agc gca acg gta aca ggg ggc cag aag ggg agg ggt tcc aga ggc      384

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64 Leu Ser Ala Thr Val Thr Gly Gly Gln Lys Gly Arg Gly Ser Arg Gly
65      115      120      125
67 caa cat caa gct cat tct ttg gag cgg gtg tgt cat tgt ttg gga aaa      432
68 Gln His Gln Ala His Ser Leu Glu Arg Val Cys His Cys Leu Gly Lys
69      130      135      140
71 tgg cta gga cat ccc gac aag ttt gtg ggc atc acc tat gcc ctg acc      480
72 Trp Leu Gly His Pro Asp Lys Phe Val Gly Ile Thr Tyr Ala Leu Thr
73 145      150      155      160
75 gtt gtg tgg ctc ctg gtg ttt gcc tgc tct gct gtg ccc gtg tac att      528
76 Val Val Trp Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile
77      165      170      175
79 tac ttc aac acc tgg acc acc tgc gac tct att gcc ttc ccc agc aag      576
80 Tyr Phe Asn Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys
81      180      185      190
83 acc tct gcc agt ata ggc agt ctc tgt gct gac gcc aga atg tat ggt      624
84 Thr Ser Ala Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly
85      195      200      205
87 gtt ctc cca tgg aat gct ttc cct ggc aag gtt tgt ggc tcc aac ctt      672
88 Val Leu Pro Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu
89      210      215      220
91 ctg tcc atc tgc aaa aca gct gag ttc caa atg acc ttc cac ctg ttt      720
92 Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe
93 225      230      235      240
95 att gct gca ttt gtg ggg gct gca gct aca ctg gtt tcc ctg ctc acc      768
96 Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr
97      245      250      255
99 ttc atg att gct gcc act tac aac ttt gcc gtc ctt aaa ctc atg ggc      816
100 Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys Leu Met Gly
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119      20      25      30
121 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu
122      35      40      45
124 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
125      50      55      60
127 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
128 65      70      75      80
130 Leu Tyr Gly Ala Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala
131      85      90      95

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133 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
134          100          105          110
136 Leu Ser Ala Thr Val Thr Gly Gly Gln Lys Gly Arg Gly Ser Arg Gly
137          115          120          125
139 Gln His Gln Ala His Ser Leu Glu Arg Val Cys His Cys Leu Gly Lys
140          130          135          140
142 Trp Leu Gly His Pro Asp Lys Phe Val Gly Ile Thr Tyr Ala Leu Thr
143 145          150          155          160
145 Val Val Trp Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile
146          165          170          175
148 Tyr Phe Asn Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys
149          180          185          190
151 Thr Ser Ala Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly
152          195          200          205
154 Val Leu Pro Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu
155          210          215          220
157 Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe
158 225          230          235          240
160 Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr
161          245          250          255
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177 <222> LOCATION: (1)..(726)
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182 1          5          10          15
184 gct tcc ctg gtg gcc act gga ttg tgt ttc ttt ggg gtg gca ctg ttc      96
185 Ala Ser Leu Val Ala Thr Gly Leu Cys Phe Phe Gly Val Ala Leu Phe
186          20          25          30
188 tgt ggc tgt gga cat gaa gcc ctc act ggc aca gaa aag cta att gag      144
189 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu
190          35          40          45
192 acc tat ttc tcc aaa aac tac caa gac tat gag tat ctc atc aat gtg      192
193 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
194          50          55          60
196 atc cat gcc ttc cag tat gtc atc tat gga act gcc tct ttc ttc ttc      240
197 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
198 65          70          75          80
200 ctt tat ggg gcc ctc ctg ctg gct gag ggc ttc tac acc acc ggc gca      288
201 Leu Tyr Gly Ala Leu Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala

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202          85          90          95
204 gtc agg cag atc ttt ggc gac tac aag acc acc atc tgc ggc aag ggc      336
205 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
206          100          105          110
208 ctg agc gca acg ttt gtg ggc atc acc tat gcc ctg acc gtt gtg tgg      384
209 Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp
210          115          120          125
212 ctc ctg gtg ttt gcc tgc tct gct gtg ccc gtg tac att tac ttc aac      432
213 Leu Leu Val Phe Ala Cys Ser Ala Val Pro Val Tyr Ile Tyr Phe Asn
214          130          135          140
216 acc tgg acc acc tgc gac tct att gcc ttc ccc agc aag acc tct gcc      480
217 Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala
218 145          150          155          160
220 agt ata ggc agt ctc tgt gct gac gcc aga atg tat ggt gtt ctc cca      528
221 Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly Val Leu Pro
222          165          170          175
224 tgg aat gct ttc cct ggc aag gtt tgt ggc tcc aac ctt ctg tcc atc      576
225 Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile
226          180          185          190
228 tgc aaa aca gct gag ttc caa atg acc ttc cac ctg ttt att gct gca      624
229 Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe Ile Ala Ala
230          195          200          205
232 ttt gtg ggg gct gca gct aca ctg gtt tcc ctg ctc acc ttc atg att      672
233 Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile
234          210          215          220
236 gct gcc act tac aac ttt gcc gtc ctt aaa ctc atg ggc cga ggc acc      720
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238 225          230          235          240
240 aag ttc tga      729
241 Lys Phe
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246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
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255          20          25          30
257 Cys Gly Cys Gly His Glu Ala Leu Thr Gly Thr Glu Lys Leu Ile Glu
258          35          40          45
260 Thr Tyr Phe Ser Lys Asn Tyr Gln Asp Tyr Glu Tyr Leu Ile Asn Val
261          50          55          60
263 Ile His Ala Phe Gln Tyr Val Ile Tyr Gly Thr Ala Ser Phe Phe Phe
264 65          70          75          80
266 Leu Tyr Gly Ala Leu Leu Leu Ala Glu Gly Phe Tyr Thr Thr Gly Ala
267          85          90          95
269 Val Arg Gln Ile Phe Gly Asp Tyr Lys Thr Thr Ile Cys Gly Lys Gly
270          100          105          110

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272 Leu Ser Ala Thr Phe Val Gly Ile Thr Tyr Ala Leu Thr Val Val Trp
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276      130      135      140
278 Thr Trp Thr Thr Cys Asp Ser Ile Ala Phe Pro Ser Lys Thr Ser Ala
279 145      150      155      160
281 Ser Ile Gly Ser Leu Cys Ala Asp Ala Arg Met Tyr Gly Val Leu Pro
282      165      170      175
284 Trp Asn Ala Phe Pro Gly Lys Val Cys Gly Ser Asn Leu Leu Ser Ile
285      180      185      190
287 Cys Lys Thr Ala Glu Phe Gln Met Thr Phe His Leu Phe Ile Ala Ala
288      195      200      205
290 Phe Val Gly Ala Ala Ala Thr Leu Val Ser Leu Leu Thr Phe Met Ile
291      210      215      220
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302 <213> ORGANISM: Homo sapiens
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305 <221> NAME/KEY: CDS
306 <222> LOCATION: (1)..(216)
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311 1      5      10      15
313 tcc aac ctt ctg tcc atc tgc aaa aca gct gag ttc caa atg acc ttc      96
314 Ser Asn Leu Leu Ser Ile Cys Lys Thr Ala Glu Phe Gln Met Thr Phe
315      20      25      30
317 cac ctg ttt att gct gca ttt gtg ggg gct gca gct aca ctg gtt tcc      144
318 His Leu Phe Ile Ala Ala Phe Val Gly Ala Ala Ala Thr Leu Val Ser
319      35      40      45
321 ctg ctc acc ttc atg att gct gcc act tac aac ttt gcc gtc ctt aaa      192
322 Leu Leu Thr Phe Met Ile Ala Ala Thr Tyr Asn Phe Ala Val Leu Lys
323      50      55      60
325 ctc atg ggc cga ggc acc aag ttc      216
326 Leu Met Gly Arg Gly Thr Lys Phe
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332 <212> TYPE: PRT
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341      20      25      30

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VERIFICATION SUMMARY

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Input Set : A:\SEQ LIST WSU-10 (US).txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date